

REMARKS

Examiner's Interview Summary

On June 24, 2008, a telephonic Examiner's Interview was conducted between Jihong Zang, Applicants' attorney, and Examiners Malgorzata Walicka and Rebecca Prouty. We thank the Examiners for their participation in the Interview. During the Interview, the enablement rejection raised in the Office Action of January 3, 2008, was discussed. The Examiners provided guidance with respect to overcoming the enablement rejection. The Examiners agreed that claims reciting chimeric polypeptides of SEQ ID NO: 5 and 8 would be acceptable. The Examiners also agreed that a polypeptide having at least 95% identity to SEQ ID NO: 8 would be acceptable. The scope of claim 3 was also discussed.

Amendments to the Claims

Claim 1 has been amended to recite "[a]n enzyme having alcohol and aldehyde dehydrogenase activity comprising an isolated polypeptide encoded by a DNA molecule according to SEQ ID NO: 4 or an isolated polypeptide with at least 95% identity to SEQ ID NO: 8." Support for this amendment may be found in the specification at, for example, page 34, line 1 to page 35, line 5; page 56, line 15 to page 60, line 24; and page 61, line 1 to page 64, line 2; and in original claim 1. See *In re Gardner*, 177 USPQ 396, 397 (CCPA 1973) and MPEP §§ 608.01(o) and (I) (8th ed. Rev. 5, August 2006, pp. 600-92 and 600-84).

Claim 2 has been amended to recite "[a]n enzyme having alcohol and aldehyde dehydrogenase activity, wherein the isolated polypeptide is a chimeric

polypeptide including a combination of at least two amino acid sequences each of said sequences being selected from the group consisting of SEQ ID NO: 5 and SEQ ID NO: 8.” Support for this amendment may be found in the specification at, for example, page 4, lines 1-6; page 13, line 23 to page 14, line 14; page 56, line 15 to page 60, line 24; and page 61, line 1 to page 64, line 2; and in original claim 2. (*Id.*)

Claim 3 has been amended to recite “[a]n enzyme of claim 1 or 2, wherein the enzyme includes at least two recombinant polypeptides in the form of a homodimer or a heterodimer.” Support for this amendment may be found in the specification at, for example, page 15, lines 21 to 26; and in original claim 3. (*Id.*)

Claim 20 has been amended to recite “[a] process for producing an aldehyde product from a substrate which comprises incubating a reaction mixture containing an enzyme of claim 1 or claim 2...” Support for this amendment may be found in the specification at, for example, page 5, lines 16 to 17 and lines 20 to 23; page 20, line 6 to page 21, line 17; page 55, lines 4-26; page 56, lines 1-14; page 58, line 9 to page 64, line 2; and in original claim 20. (*Id.*)

Claim 21 has been amended to recite “[a] process for producing a ketone product from a substrate which comprises incubating a reaction mixture containing an enzyme of claim 1 or claim 2...” Support for this amendment may be found in the specification at, for example, page 5, lines 16 to 17 and lines 20 to 23; page 20, line 6 to page 21, line 17; page 55, lines 4-26; page 56, lines 1-14; page 58, line 9 to page 64, line 2; and in original claim 21. (*Id.*)

Claim 22 has been amended to recite “[a] process for producing a carboxylic acid product from a substrate which comprises incubating a reaction mixture containing an enzyme of claim 1 or claim 2...” Support for this amendment may be found in the specification at, for example, page 5, lines 16 to 17 and lines 20 to 23; page 20, line 6 to page 21, line 17; page 55, lines 4-26; page 56, lines 1-14; page 58, line 9 to page 64, line 2; and in original claim 22. (*Id.*)

Claim 25 has been amended to recite “[a] process for producing 2-keto-L-gulonic acid which comprises: (a) incubating a reaction mixture containing a substrate selected from the group consisting of D-sorbitol and L-sorbose, and an enzyme according to claim 1 or claim 2...” Support for this amendment may be found in the specification at, for example, page 13, lines 19 to 21; page 21, lines 4 to 17; page 33, Table 6; page 54, line 16 to page 55, line 26; and page 62, line 1 to page 64, line 2; and in original claim 25. (*Id.*)

Claim 30 has been amended to recite “[a]n isolated enzyme having alcohol and aldehyde dehydrogenase activity encoded by a recombinant expression vector comprising a DNA sequence of SEQ ID NO: 4 or a DNA sequence which encodes a polypeptide with at least 95% identity to SEQ ID NO: 8...” Support for this amendment may be found in the specification at, for example, page 34, line 1 to page 35, line 5; page 56, line 15 to page 60, line 24; and page 61, line 1 to page 64, line 2; and in original claim 30. (*Id.*)

Claim 31 has been amended to recite “[a]n isolated enzyme having alcohol and aldehyde dehydrogenase activity encoded by a recombinant expression vector comprising a DNA sequence of SEQ ID NO: 4 or a DNA sequence which

encodes a polypeptide with at least 95% identity to SEQ ID NO: 8.” Support for this amendment may be found in the specification at, for example, page 34, line 1 to page 35, line 5; page 56, line 15 to page 60, line 24; and page 61, line 1 to page 64, line 2; and in original claim 31. (*Id.*)

Claims 32 and 33 have been added. Support for these claims may be found in the specification at, for example, page 34, line 1 to page 35, line 5; and in original claims 30 and 31, respectively. (*Id.*)

Claims 34 and 35 have been added. Support for these claims may be found in the specification at, for example, page 56, line 15 to page 60, line 24; and page 61, line 1 to page 64, line 2; and in original claims 30 and 31, respectively. (*Id.*)

Claims 36 has been added. Support for this claim may be found in original claims 1 and 20, and in the specification at, for example, page 5, lines 16 to 17 and lines 20 to 23; and page 20, line 6 to page 21, line 17. (*Id.*)

Claim 37 has been added. Support for this claim may be found in original claims 1 and 21, and in the specification at, for example, page 5, lines 16 to 17 and lines 20 to 23; and page 20, line 6 to page 21, line 17. (*Id.*)

Claim 38 has been added. Support for this claim may be found in original claims 1 and 22, and in the specification at, for example, page 5, lines 16 to 17 and lines 20 to 23; and page 20, line 6 to page 21, line 17. (*Id.*)

Claim 39 has been added. Support for this claim may be found in original claims 1 and 25, and in the specification at, for example, page 13, lines 19 to 21; page 21, lines 4 to 17; and page 33, Table 6. (*Id.*)

It is submitted that no new matter has been introduced by the foregoing amendments. Moreover, the claim amendments and additions are made to place the application in condition for allowance or better form for appeal, and, are thus appropriate. Approval and entry of the amendments and claim additions are respectfully solicited.

Enablement Rejection

A. Claims 1-3, 20-22, 25, 28, 30-31

Claims 1-3, 20-22, 25, 28, and 30-31 were rejected solely under 35 USC §112, first paragraph, on the asserted grounds that the specification is not enabling (Paper No. 20071221, at 2).

In making the rejection, the Examiner asserted that the specification “does not reasonably provide enablement for any amino acid sequence comprising a sequence that has at least 90% identity to SEQ ID NO: 8.” (*Id.*, emphasis original). The Examiner, however, acknowledges that the specification is “enabling for the alcohol and aldehyde dehydrogenase of SEQ ID NO: 5, 6, 7, and 8.” (*Id.*)

The Examiner further asserted that “[h]aving 90% identity, i.e. having 58 random mutations in the protein of 579 amino acids, imposes on a skilled artisan an extremely lengthy experimentation that is undue.” (*Id.*) The Examiner further asserted that Guo *et al.*, “Protein Tolerance to Random Amino Acid Change,” *Proc Natl Acad Sci U S A*, 101 (25): 9205-10 (2004) (“Guo”) discloses that “the fraction of random single substitution mutations which inactivate a protein of about 300 amino acid (human 3-methyladenine DNA glycosylase) is 0.34 and that this number appears to be consistent

with other studies in other proteins as well.” (*Id.* at 2-3). Additionally, the Examiner asserted that Guo “further show[ed] in Table 1 and formula 1[] on page 9206 left column, that the fraction of active mutants for multiple mutations may be roughly estimated by formula $(1-0.34)^n$ where n is the number of mutations introduced.” (*Id.* at 3). Applying Guo’s formula, the Examiner asserted that “58 mutations of SEQ ID NO: 8 or SEQ ID NO: 5, gives ... $(.66)^{58}$ ie., 3.42×10^{-12} of random mutants being active.” (*Id.*) Although the Examiner acknowledged that “current techniques... in the art would allow for finding a few active mutants within about a million inactive mutants as is the case for the claims limited to 95% identity,” the Examiner asserted that “finding a few mutants within hundreds of billions (exactly 2.9×10^{11} in the case at hand) as in the claims to 90% or less identity would not be possible without undue experimentation, especially that the presented calculation relates to viable mutants only.” (*Id.*) The Examiner also asserted, “[w]hile enablement is not precluded by the necessity for routine screening, if a large amount of screening is required, the specification must provide a reasonable amount of guidance with respect to the direction in which the experimentation should proceed.” (*Id.*) The Examiner further asserted that “[s]uch guidance has not been provided in the instant specification.” (*Id.*) Additionally, the Examiner asserted that “not only is the quantity of experimentation overwhelming in the instant situation but the specification provides no guidance with regard to what variants to make in order to reduce the amount of experimentation to a reasonable level.” (*Id.* at 3-4) The Examiner further asserted that “[a]pplicants do not teach in details how to modify SEQ ID NO: 8 so that the modified protein, having 58 mutations was still having the same

enzymatic activity as the parental one.” (*Id.* at 4) The Examiner then concluded that “[i]n summary, the claims are rejected.” (*Id.*)

The Federal Circuit, adopting the analysis set forth in *Ex parte Forman*, 230 USPQ 546 (BPAI 1986), has enumerated several factors which may be considered in determining whether claims require that one skilled in the art perform undue experimentation in order to practice the claimed subject matter: breadth of the claims; predictability or unpredictability of the art; relative skill of those in the art; state of the prior art; nature of the invention; working examples; amount of guidance; and quantity of experimentation necessary. *In re Wands*, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). These factors are merely illustrative, not mandatory; they provide a general framework for analysis. *Enzo Biochem v. Calgene Inc.*, 188 F.3d 1362, 1371, 52 USPQ2d 1129, 1136 (Fed. Cir. 1999); *Amgen, Inc. v. Chugai Pharm. Co.*, 927 F.2d 1200, 1213, 18 USPQ2d 1016, 1027 (Fed. Cir.), *cert. denied*, 502 U.S. 856 (1991).

With a view towards furthering prosecution and as instructed by the Examiners during the interview, claims 1, 30 and 31 have been amended to recite “...or an isolated polypeptide with at least 95% identity to SEQ ID NO: 8.”

As acknowledge by the Examiner, the disclosed polypeptide is 579 amino acids. Therefore, a recitation of 95% identity to SEQ ID NO: 8 means 29 mutations, and thus the claim is not overly broad.

Furthermore, as the Examiner acknowledged, “[c]urrent techniques (i.e., high throughput mutagenesis and screening techniques) in the art would allow for finding a few active mutants within about a million inactive mutants” (Paper No. 20071221 at 3). Thus, the Examiner appears to concede that the relative skill of a

person skilled in the art is high, the art of mutagenesis and screening is fairly predictable, and the state of the prior art is reasonably advanced.

Additionally, the specification provides ample disclosure sufficient to make, screen and use a variant of alcohol and aldehyde dehydrogenase. The specification discloses, *inter alia*, how to isolate and clone DNA of interest, how to construct the mutants, and how to test the function of putative alcohol and aldehyde dehydrogenase. (See, e.g., examples 4-7 and 14-15). Given the disclosure, a person skilled in the art would be able to make enzyme B (SEQ ID NO. 8) and assay it for alcohol and aldehyde dehydrogenase function.

Moreover, the specification of the instant application provides guidance as to what amino acid substitutions may be made without altering alcohol and aldehyde dehydrogenase function. For example, page 14, lines 20 to 26 of the specification discloses,

[a]mino acid exchanges in proteins and peptides which do not generally alter the activity of such molecules are known in the state of the art and are described, for example, by H. Neurath and R.L. Hill in "The Proteins"... The most commonly occurring exchanges are: Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, Asp/Gly as well as these exchanges in reverse.

Thus, the specification provides specific guidance to appropriate amino acid substitutions.

The specification also provides sixteen working examples of enzymes alcohol and aldehyde dehydrogenase activity besides enzyme B (SEQ ID NO: 8). Example 2 discloses three other alcohol and aldehyde dehydrogenases, which share

81 to 89% identity with enzyme B. Furthermore, example 14 discloses thirteen additional examples of chimeric proteins obtained by exchanging different portions of enzyme A (SEQ ID NO: 5) and enzyme B: A/B1, A/B3, A/B21, A/B22, A/B25, sA21, sA22, sA2, B/A1, B/A2, B/A3, A/B31, and sB. Two different methods of making these variants of enzyme B were also disclosed in that example: the common restriction sites method and the *in vivo* homologous recombination method. These variants share 85% to 96% identity with enzyme B, as analyzed by BLAST and set forth in the table below. (The BLAST comparison results are shown in the attached Exhibit 1.) These experiments provide clear guidance as to what amino acid substitutions may be made.

Polypeptide name (as given in the specification)	Percent identity with SEQ ID NO: 8
A/B1	92%
A/B3	89%
A/B21	95%
A/B22	95%
A/B25	94%
sA21	85%
sA22	86%
sA2	85%
B/A1	89%
B/A2	92%
B/A3	93%
A/B31	96%
sB	86%

Finally, we address the Examiner's arguments with respect to the Guo disclosure. Initially, we note that while the formula for the percentage of active mutants for multiple mutations cited by the examiner, $(0.66)^x$, wherein x is the number of mutations introduced, is applicable to human 3-methyladenine DNA glycosylase (AAG), the 0.66 value used in the formula varies significantly across various proteins, ranging

from 0.44 to as high as 0.81. (See e.g., Guo, page 9206, column 2, lines 27-30 and table 2). Furthermore, Guo discloses that “[t]here likely are variations in the substitutability of different proteins.” (Guo, page 9207, column 1, lines 32-33.) Hence, the formula cited by the Examiner is not likely to be applicable to the alcohol and aldehyde dehydrogenase disclosed by the present application. And, indeed the Examiner has provided no evidence that such a formula would be relevant in the present context.

Furthermore, even assuming that the formula, $(0.66)^x$, accurately describes the percentage of active mutants for multiple mutations in the alcohol and aldehyde as disclosed by the Applicants, the amended claim 1 still would be enabling. The disclosed alcohol and aldehyde dehydrogenase is a polypeptide of 579 amino acids, and 95% amino acid sequence identity means a mutation of only about 29 amino acids. Using the formula above, $(0.66)^{29}$ gives 5.8×10^{-6} . This number, which translates to 1 in 171,090, is well within the Examiner’s acknowledged ability of the current art, which “allow for finding a few active mutants within about a million inactive mutants.” (Paper No. 20071221 at 3). Given that guidance is provided in the specification as to what substitution of amino acids may be made without altering the enzymatic activities, the probability of 1 in 171,090 should be further increased, and again, well within the ability of the current art.

At bottom, the amount of experimentation required to achieve 95% identity with a DNA encoding a polypeptide which comprises the amino acid sequence of SEQ ID NO: 8, and encodes an enzyme with alcohol and aldehyde dehydrogenase is not undue, particularly given that the Examiner appears to concede that the techniques of

mutation are well developed in the art, that the skill of artisans in this field is high, the capacity of the current mutant screens is large, and that the specification includes assays and working examples as to how to assess the function of alcohol and aldehyde dehydrogenase, as well as guidance to nucleotide changes.

Therefore, we respectfully submit as amended, claims 1, 30 and 31 and their dependent claims are enabling. Accordingly, the rejection has been rendered moot and should be withdrawn.

B. Claims 2 and 3

Claims 2 and 3 were “specifically rejected” under 35 U.S.C. 112, first paragraph on the asserted grounds that the specification is not enabling (Paper No. 20071221, at 4).

In making the rejection, the Examiner asserted that the specification “does not reasonably provide enablement for an enzyme that comprises a combination of at least two amino acids sequences each of said sequences being selected from the group of SEQ ID NO: 8 and SEQ ID NO: 5 and amino acid sequences that are at least 90% identical to SEQ ID NO: 8 or SEQ ID NO: 5.” (*Id.*, emphasis original). The Examiner asserted that “the reasons for this rejection were explained in the previous actions.” The Examiner also asserted that “[t]he main conclusion has been: without a further guidance on the part of Applicants related to the structure of chimeric enzymes, one skilled in the art is forced to construct numerous combination [*sic*] of disclosed sequences or sequences that are at least 90% homologous to them, express the chimeric proteins, [and] examine the enzymatic activity of the expressed constructs with a low probability of success.” (*Id.*) The Examiner then concluded, “[t]hus the

experimentation left to those in the art is undue.” (*Id.*) The Examiner, however, acknowledged that the specification is “enabling for the plasmid comprising genes encoding SEQ ID NO: 5 and SEQ ID NO: 8 (plasmids pSSAB201 and pSSBA201).” (*Id.*)

With a view towards furthering prosecution, claim 2 has been amended to recited “[a]n enzyme having alcohol and aldehyde dehydrogenase activity, wherein the isolated polypeptide is a chimeric polypeptide including a combination of at least two amino acid sequences each of said sequences being selected from the group consisting of SEQ ID NO: 5 and SEQ ID NO: 8.” As set forth above in the previous section, the specification has provided 13 working examples of chimeric polypeptides including a combination of at least two amino acid sequences from SEQ ID NOs: 5 and 8, as well as methods of making these chimera, methods of assay for their activity, and how to use them. (Example 14 and 15, pages 56-64) Therefore, claim 2, as amended, is enabling.

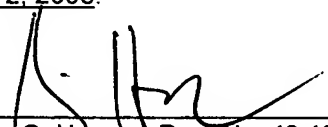
Because claim 3, as amended, depends from claims 1 and 2, claim 3 incorporates the language of claims 1 and 2, and thus is enabling as well.

Accordingly, it is respectfully submitted that the “specific rejection” has been rendered moot and should be withdrawn.

Application No.: 10/802,682
Amendment Dated: July 2, 2008
Reply to Office Action Dated: January 3, 2008

For the reasons set forth above, entry of the amendments, reconsideration, withdrawal of the rejection, and allowance of the claims are respectfully requested. If the Examiner has any questions regarding this paper, please contact the undersigned.

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Mail Stop AF, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on July 2, 2008.



Kevin C. Hooper, Reg. No. 40,402

Respectfully submitted,

By: 

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

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☐ Show CDS translation Align

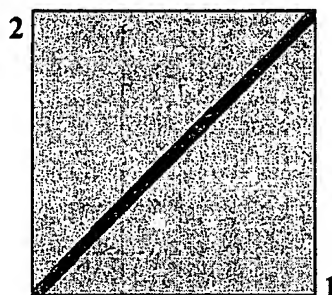
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Sequence 2: unnamed protein product

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

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☐ Show CDS translation Align

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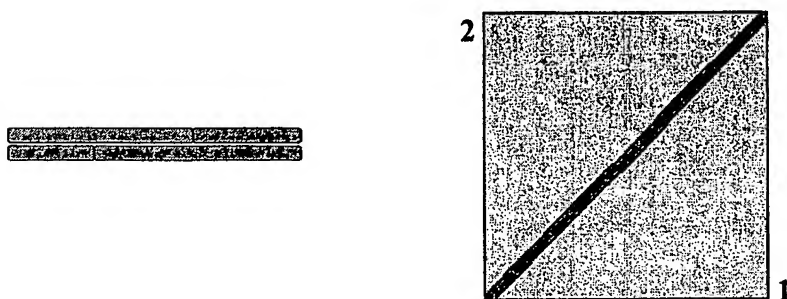
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 579 (1 .. 579)

1: B

2: A/B3



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



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Query	540	QYIAIGAGGLTYGTQLNAPLAEIDSTSVGNAIYVFALPQ	579
		QYIAIGAGGLTYGTQLNAPLAEIDSTSVGNAIYVFALPQ	
Sbjct	540	QYIAIGAGGLTYGTQLNAPLAEIDSTSVGNAIYVFALPQ	579

CPU time: 0.04 user secs. 0.04 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

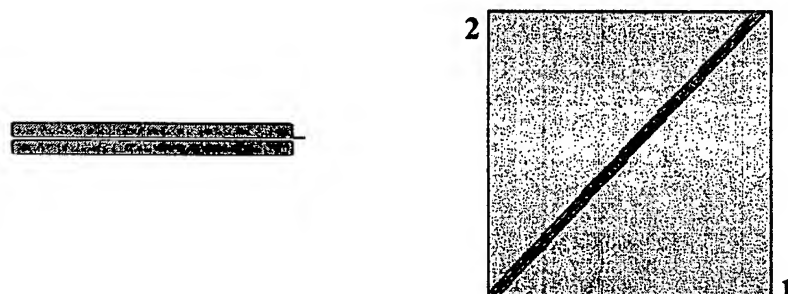
Length = 579 (1 .. 579)

1: B

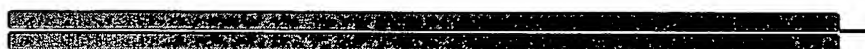
Sequence 2: unnamed protein product

Length = 556 (1 .. 556)

2: A/B21



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1100 bits (2844), Expect = 0.0

Identities = 531/556 (95%), Positives = 542/556 (97%), Gaps = 0/556 (0%)

Query	1	MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAFAQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQA+DA+TGDLIWEHRRQLP	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPN	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGSGEDGLTSNTTGP	180
		+ATLN+ GDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGSGEDGLTSNTTGP	
Sbjct	121	IATLNSFGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGC FISGHDSATGEELWRNHFI PQPGEEGDET WGND FEARWMT	240
		IVANGVIVAGSTCQYSPYGC FISGHDSATGEELWRNHFI PQPGEEGDET WGND FEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPYGC FISGHDSATGEELWRNHFI PQPGEEGDET WGND FEARWMT	240

```
Query  241  GVWQGITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQL 300
          GVWQGITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQL
Sbjct  241  GVWQGITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQL 300

Query  301  PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSDAA 360
          PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSDAA
Sbjct  301  PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSDAA 360

Query  361  SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP 420
          SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP
Sbjct  361  SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP 420

Query  421  TGIYFLPLNNACYDIMAVDQEFSALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA 480
          TGIYFLPLNNACYDIMAVDQEFSALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA
Sbjct  421  TGIYFLPLNNACYDIMAVDQEFSALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA 480

Query  481  ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDGVS 540
          ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDGVS
Sbjct  481  ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDGVS 540

Query  541  YIAIGAGGLTYGTQLN 556
          YIAIGAGGLTYGTQLN
Sbjct  541  YIAIGAGGLTYGTQLN 556
```

CPU time: 0.04 user secs. 0.04 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align**Sequence 1:** unnamed protein product

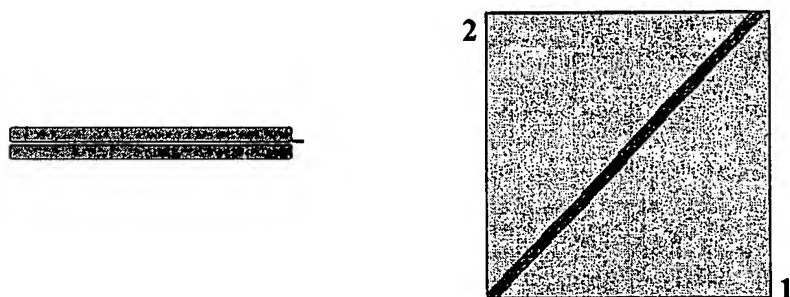
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 556 (1 .. 556)

1: B

2: A/B22



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1104 bits (2855), Expect = 0.0
Identities = 533/556 (95%), Positives = 543/556 (97%), Gaps = 0/556 (0%)

Query	1	MNPTTLRLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAFQVTPVTDELLANPPAGEWISYQONQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPMIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQA+DA+TGDLIWEHRRQLP	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPN	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVERGSGEDGLTSNTTGP	180
		+ATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVERGSGEDGLTSNTTGP	
Sbjct	121	IATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFI PQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFI PQPGEEGDETGWGNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFI PQPGEEGDETGWGNDFEARWMT	240

Query	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
		GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	
Sbjct	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
Query	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	360
		PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	
Sbjct	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	360
Query	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP	420
		SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP	
Sbjct	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP	420
Query	421	TGIYFLPLNNACYDIMAVDQEFSAALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWS	480
		TGIYFLPLNNACYDIMAVDQEFSAALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWS	
Sbjct	421	TGIYFLPLNNACYDIMAVDQEFSAALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWS	480
Query	481	ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG	540
		ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG	
Sbjct	481	ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG	540
Query	541	YIAIGAGGLTYGTQLN	556
		YIAIGAGGLTYGTQLN	
Sbjct	541	YIAIGAGGLTYGTQLN	556

CPU time: 0.04 user secs. 0.05 sys. secs 0.09 total secs.

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align**Sequence 1:** unnamed protein product

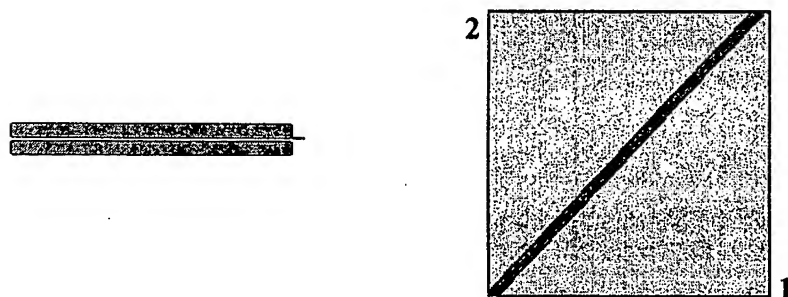
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 556 (1 .. 556)

1: B

2: A/B25



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1092 bits (2824), Expect = 0.0
Identities = 527/556 (94%), Positives = 540/556 (97%), Gaps = 0/556 (0%)

Query	1	MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAFQVTPVTDELLANPPAGEWISYQONQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPMIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQA+DA+TGDLIWEHRRQLP	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPN	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFDFVERGSGEDGLTSNTTGP	180
		+ATLN+ G+ RG+ALYGTSLYFSSWDNHLIALDMETGQVVFDFVERGSGEDGLTSNTTGP	
Sbjct	121	IATLNSFGPEPTRGMALYGTSLYFSSWDNHLIALDMETGQVVFDFVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240

Query	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQL	300
		GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQL	
Sbjct	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQL	300
Query	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	360
		PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	
Sbjct	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	360
Query	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP	420
		SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP	
Sbjct	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP	420
Query	421	TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAIIDISTGRTLWS	480
		TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAIIDISTGRTLWS	
Sbjct	421	TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAIIDISTGRTLWS	480
Query	481	ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG	540
		ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG	
Sbjct	481	ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG	540
Query	541	YIAIGAGGLTYGTQLN	556
		YIAIGAGGLTYGTQLN	
Sbjct	541	YIAIGAGGLTYGTQLN	556

CPU time: 0.04 user secs. 0.03 sys. secs 0.07 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

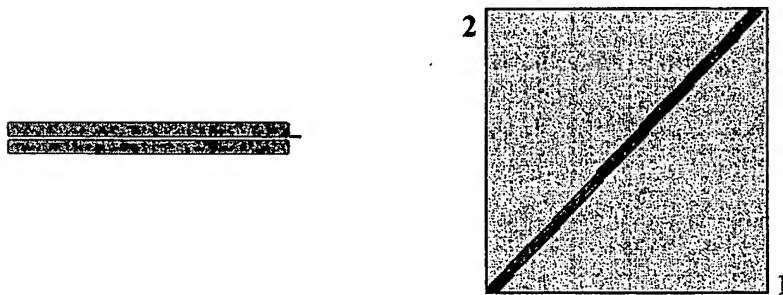
Length = 579 (1 .. 579)

1: B

Sequence 2: unnamed protein product

Length = 557 (1 .. 557)

2: SA 21



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1013 bits (2620), Expect = 0.0

Identities = 478/557 (85%), Positives = 516/557 (92%), Gaps = 0/557 (0%)

Query	1	MNPTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAFQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPMIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQA+DA+TGDLIWEHRRQLP	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPN	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
		+ATLN+ GDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	
Sbjct	121	IATLNSFGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGCFIGSHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSP+GCF+SGHDSATGEELWRN+FIP+ GEEGDETGWGNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFIPRAGEEGDETGWGNDEARWMT	240

Query	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
		G WGQITYDPVTNLV YGST VGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	
Sbjct	241	GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
Query	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA	360
		PRDNWDQECTFEMMV NVDVQPS EMEGL++INPNAATGERRVLTG PCKTGTMW FDA	
Sbjct	301	PRDNWDQECTFEMMVTNVDVQPSSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAE	360
Query	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD	420
		+GEFLWARDTNY NMI SIDE G+VTVNEDA+LKELDVEYDVCPTFLGGRDW SAALNPD	
Sbjct	361	TGEFLWARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPD	420
Query	421	TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA	480
		+GIYF+PLNN CYD+MAVDQEF+++DVYNTS KL PG + +GRIDAIDISTGRTLWS	
Sbjct	421	SGIYFIPLNNVCYDMMAVDQEFSSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV	480
Query	481	ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDGVO	540
		ER AANYSPVLST GGV+FNGGTDYFRALSQETGETLWQ RLATVA+GQAISYE+DG+Q	
Sbjct	481	ERAAANYSPVLSTGGGVLFNGGTDYFRALSQETGETLWQTRLATVASGQAISYEVDGMQ	540
Query	541	YIAIGAGGLTYGTQLNA	557
		Y+AI GG++YG+ LN+	
Sbjct	541	YVAIAGGGVSYGSGLNS	557

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

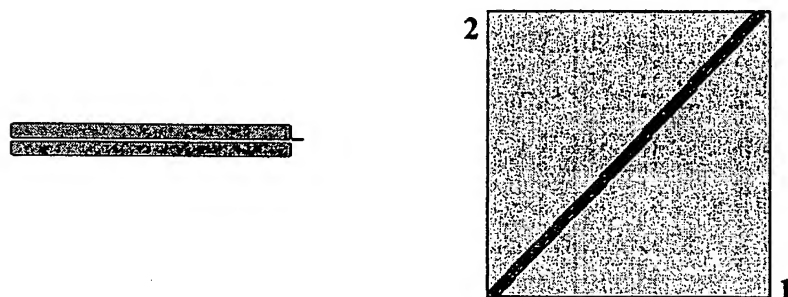
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 557 (1 .. 557)

1: B

2: SA 22



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1018 bits (2631), Expect = 0.0

Identities = 480/557 (86%), Positives = 517/557 (92%), Gaps = 0/557 (0%)

Query	1	MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLWASAGALALLAAPAFQVTPVTDELLANPPAGEWISYQONQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQA+DA+TGDLIWEHRRQLP	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPN	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVDVERGSGEDGLTSNTTGP	180
		+ATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVDVERGSGEDGLTSNTTGP	
Sbjct	121	IATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVDVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGCFFISGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSP+GCF+SGHDSATGEELWRN+FIP+ GEEGDETGWGN+EARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFIPRAGEEGDETGWGNDEARWMT	240

```
Query 241  GVWQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT 300
           G WGQITYDPVTNLV YGST VGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT
Sbjct 241  GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT 300

Query 301  PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAAATGERRVLTGAPCKTGTMWSFDA 360
           PRDNWDQECTFEMMV NVDVQPS EMEGL++INPNAAATGERRVLTG PCKTGTMW FDA
Sbjct 301  PRDNWDQECTFEMMVTVNVDVQPSTEMEGLQSINPNAAATGERRVLTGVPCKTGTMWQFDAE 360

Query 361  SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD 420
           +GEFLWARDTNY NMI SIDE G+VTVNEDA+LKELDVEYDVCPTFLGGRDW SAALNPD
Sbjct 361  TGEFLWARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPD 420

Query 421  TGIYFLPLNNACYDIMAVDQEFSA LDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA 480
           +GIYF+PLNN CYD+MAVDQEF+++DVYNTS KL PG + +GRIDAIDISTGRTLWS
Sbjct 421  SGIYFIPLNNVCYDMMAVDQEFTSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV 480

Query 481  ERPAANYSPVLSTAGGVFENG GTDRYFRALSQETGETLWQARLATVATGQAISYELDG VQ 540
           ER AANYSPVLST GGV+FENG GTDRYFRALSQETGETLWQ RLATVA+GQAISYE+DG+Q
Sbjct 481  ERAAANYSPVLSTGGGVLFENG GTDRYFRALSQETGETLWQTRLATVASGQAISYEVDGMQ 540

Query 541  YIAIGAGGLTYGTQLNA 557
           Y+AI GG++YG+ LN+
Sbjct 541  YVAIAGGGVSYGSGLNS 557
```

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

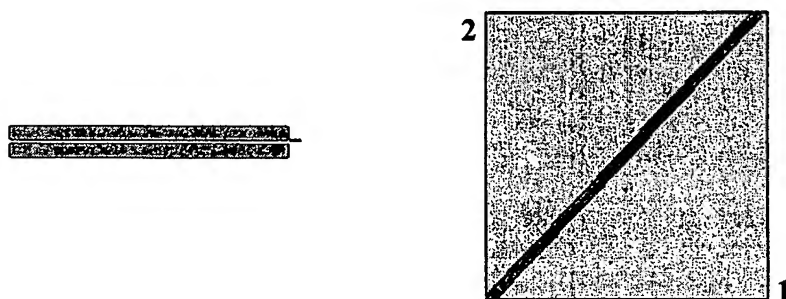
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 557 (1 .. 557)

1: B

2: SA2



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1006 bits (2600), Expect = 0.0
 Identities = 474/557 (85%), Positives = 514/557 (92%), Gaps = 0/557 (0%)

Query	1	MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAAFAQVTPVTDDELLANPPAGEWISYQONQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQA+DA+TGDLIWEHRRQLP	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQAIDAKTGDLIWEHRRQLPN	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGSGEDGLTSNTTGP	180
		+ATLN+ G+ RG+ALYGTSLYFSSWDNHLIALDMETGQVVF DVERGSGEDGLTSNTTGP	
Sbjct	121	IATLNSFGPEPTRGMALYGTSLYFSSWDNHLIALDMETGQVVF DVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGCFFISGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSP+GCF+SGHDSATGEELWRN+FIP+ GEEGDETGWGND+EARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFIPRAGEEGDETGWGNDYEARWMT	240

Query	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
		G WGQITYDPVTNLV YGST VGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	
Sbjct	241	GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
Query	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAAATGERRVLTGAPCKTGTMWSFDAA	360
		PRDNWDQECTFEMMV NVDVQPS EMEGL++INPNAAATGERRVLTG PCKTGTMW FDA	
Sbjct	301	PRDNWDQECTFEMMVTNVDVQPSSTEMEGLQSINPNAAATGERRVLTGVPCKTGTMWQFDAE	360
Query	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD	420
		+GEFLWARDTNY NMI SIDE G+VTVNEDA+LKELDVEYDVCPTFLGGRDW SAALNPD	
Sbjct	361	TGEFLWARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPD	420
Query	421	TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA	480
		+GIYF+PLNN CYD+MAVDQEF+++DVYNTS KL PG + +GRIDAIDISTGRTLWS	
Sbjct	421	SGIYFIPLNNVCYDMMAVDQEFSSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV	480
Query	481	ERPAANYSPVLSTAGGVFENGTDYFRALSQETGETLWQARLATVATGQAISYELDGVO	540
		ER AANYSPVLST GGV+FENGTDYFRALSQETGETLWQ RLATVA+GQAISYE+DG+Q	
Sbjct	481	ERAAANYSPVLSTGGGVLFENGTDYFRALSQETGETLWQTRLATVASGQAISYEVDGMQ	540
Query	541	YIAIGAGGLTYGTQLNA	557
		Y+AI GG++YG+ LN+	
Sbjct	541	YVAIAGGGVSYGSLNS	557

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

Length = 579 (1 .. 579)

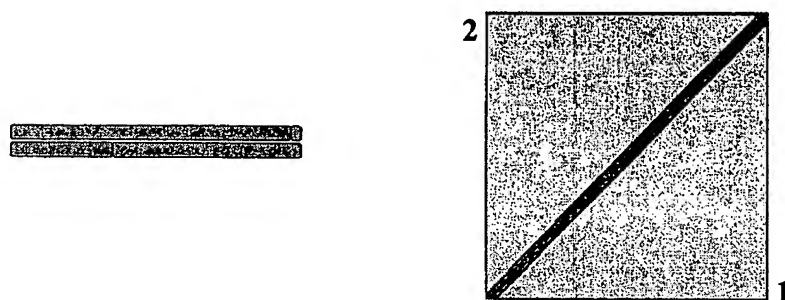
Sequence 2: unnamed protein product

Length = 579 (1 .. 579)

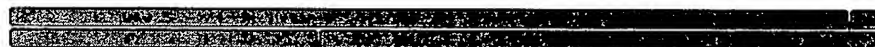
SEQ 1 : B

- vs.

SEQ 2 : B/A1



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1082 bits (2799), Expect = 0.0

Identities = 520/580 (89%), Positives = 549/580 (94%), Gaps = 2/580 (0%)

Query	1	MNPTTLLRTSAAVLLLTPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		MNPTTLLRTSAAVLLLTPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	
Sbjct	1	MNPTTLLRTSAAVLLLTPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	
Sbjct	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGS GEDGLTSNTTGP	180
		VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGS GEDGLTSNTTGP	
Sbjct	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVF DVERGS GEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGC FIGHDSATGEELWRNHFI PQPGEEGDET WGNDFEARWMT	240
		IVANGVIVAGSTCQYSPYGC FIGHDSATGEELWRN+ FIP+ GEEGDET WGNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPYGC FIGHDSATGEELWRNYFIPRAGEEGDET WGNDFEARWMT	239

Query 241 GVWQGITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT 300
G WGQITYDPVTNLV YGST VGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT
Sbjct 240 GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT 299

Query 301 PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAAATGERRVLTGAPCKTGTMWSFDAA 360
PRDNWDQECTFEMMV NVDVQPS EMEGL++INPNAAATGERRVLTG PCKTGTMW FDA
Sbjct 300 PRDNWDQECTFEMMVTVNDVQPSSTEMEGLQSINPNAAATGERRVLTGVPCKTGTMWQFDAE 359

Query 361 SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD 420
+GEFLWARDTNY NMI SIDE G+VTVNEDA+LKELDVEYDVCPTFLGGRDW SAAALNPD
Sbjct 360 TGEFLWARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPD 419

Query 421 TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA 480
+GIYF+PLNN CYD+MAVDQEF+++DVYNTS KL PG + +GRIDAIDISTGRTLWS
Sbjct 420 SGIYFIPLNNVCYDMMAVDQEFSSMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV 479

Query 481 ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG VQ 540
ER AANYSPVLST GGV+FNNGGTDYFRALSQETGETLWQ RLATVA+GQAISYE+DG+Q
Sbjct 480 ERAAANYSPVLSTGGGVLFNGGTDYFRALSQETGETLWQTRLATVASGQAISYEV DGMQ 539

Query 541 YIAIGAGGLTYGTQLNAPLA-EAIDSTSVGNAIYVFALPQ 579
Y+AI GG++YG+ LN+ LA E +DST++GNA+YVFALPQ
Sbjct 540 YVAIAGGGVSYGSLNSALAGERVDSTAIGNAVYVFALPQ 579

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.000(wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align**Sequence 1:** unnamed protein product

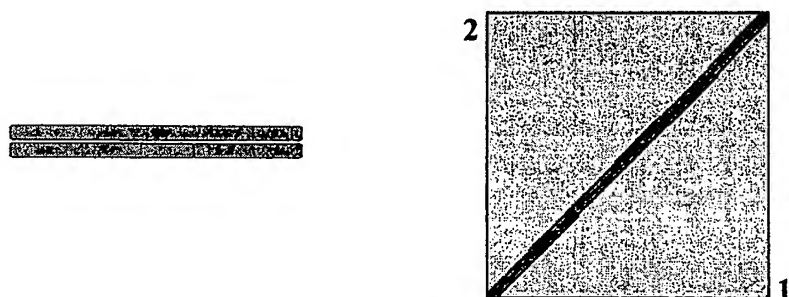
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 579 (1 .. 579)

1 : B

2 : B/A2



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1108 bits (2866), Expect = 0.0
Identities = 535/580 (92%), Positives = 558/580 (96%), Gaps = 2/580 (0%)

Query	1	MNPTLLRTSAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		MNPTLLRTSAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	
Sbjct	1	MNPTLLRTSAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	
Sbjct	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
		VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	
Sbjct	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240

Query	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
		GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	
Sbjct	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
Query	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDAA	360
		PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDAA	
Sbjct	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDAA	360
Query	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD	420
		SGE LWARDTNY NMI SIDE G+VTVNEDA+LKELDVEYDVCPTFLGGRDW SAALNPD	
Sbjct	361	SGE-LWARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNPD	419
Query	421	TGIYFLPLNNACYDIMAVDQEFSAALDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWSA	480
		+GIYF+PLNN CYD+MAVDQEF+++DVYNTS KL PG + +GRIDAIDISTGRTLWS	
Sbjct	420	SGIYFIPLNNVCYDMMAVDQEFSTMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV	479
Query	481	ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDGVQ	540
		ER AANYSPVLST GGV+FNGGTDYFRALSQETGETLWQ RLATVA+GQAISYE+DG+Q	
Sbjct	480	ERAAANYSPVLSTGGGVLFNGGTDYFRALSQETGETLWQTRLATVASGQAISYEVDGMQ	539
Query	541	YIAIGAGGLTYGTQLNAPLA-EAIDSTSVGNAIYVFALPQ	579
		Y+AI GG++YG+ LN+ LA E +DST++GNA+YVFALPQ	
Sbjct	540	YVAIAGGGVSYGSLNSALAGERVDSTAIGNAVYVFALPQ	579

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

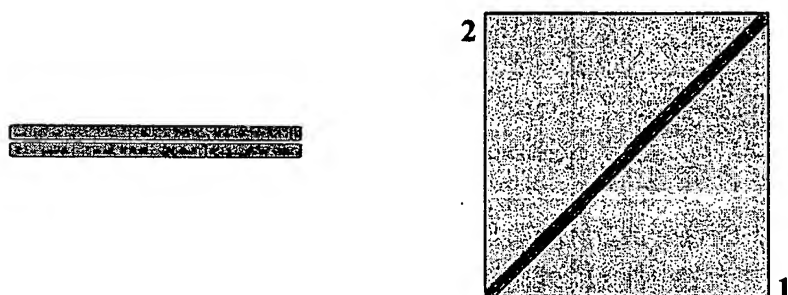
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

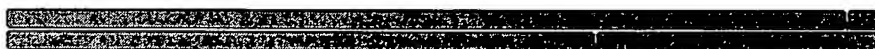
Length = 579 (1 .. 579)

1: B

2: B/A3



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1116 bits (2887), Expect = 0.0

Identities = 540/580 (93%), Positives = 561/580 (96%), Gaps = 2/580 (0%)

Query	1	MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	
Sbjct	1	MNPTTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	
Sbjct	61	ADNVGQLQLVWARGMEAGAVQVTPIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
		VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	
Sbjct	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240

```
Query 241 GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT 300
          GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT
Sbjct 241 GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT 300

Query 301 PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA 360
          PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA
Sbjct 301 PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA 360

Query 361 SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP 420
          SGEFLWARDTNYTNMIASIDETGLVTVNEDA LKELDVEYDVCPTFLGGRDW SAALNP
Sbjct 361 SGEFLWARDTNYTNMIASIDETGLVTVNEDA-LKELDVEYDVCPTFLGGRDWPSAALNP 419

Query 421 TGIYFLPLNNACYDIMAVDQEFSA LDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWS 480
          +GIYF+PLNN CYD+MAVDQEF+++DVYNTS KL PG + +GRIDAIDISTGRTLWS
Sbjct 420 SGIYFIPLNNVCYDMMAVDQEFSTMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV 479

Query 481 ERPAANYSPVLSTAGGVVFNGGTDYFRALSQETGETLWQARLATVATGQAISYELDG 540
          ER AANYSPVLST GGV+FNGGTDYFRALSQETGETLWQ RLATVA+GQAISYE+DG+Q
Sbjct 480 ERAAANYSPVLSTGGGVLFNGGTDYFRALSQETGETLWQTRLATVASGQAISYEV 539

Query 541 YIAIGAGGLTYGTQLNAPLA-EAIDSTSVGNAIYVFALPQ 579
          Y+AI GG++YG+ LN+ LA E +DST++GNA+YVFALPQ
Sbjct 540 YVAIAGGGVSYGSLNSALAGERVDSTAIGNAVYVFALPQ 579
```

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

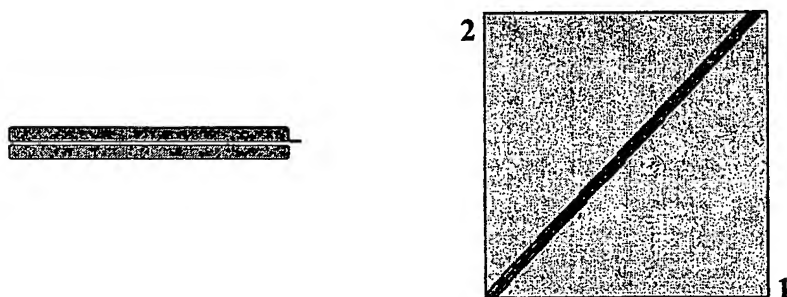
☐ Show CDS translation Align**Sequence 1:** unnamed protein product

Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

Length = 556 (1 .. 556)

1: B

2: ~~B~~ A/B31

NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1109 bits (2868), Expect = 0.0

Identities = 537/556 (96%), Positives = 544/556 (97%), Gaps = 0/556 (0%)

Query	1	MNPTLLRTSAAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAAFAQVTPVITDELLANPPAGEWISYQGNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPMIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVERGSGEDGLTSNTTGP	180
		VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVERGSGEDGLTSNTTGP	
Sbjct	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVFVERGSGEDGLTSNTTGP	180
Query	181	IVANGVIVAGSTCQYSPYGC FISGHSATGEELWRNHFI PQPGEEGDETGWNDFEARWMT	240
		IVANGVIVAGSTCQYSPYGC FISGHSATGEELWRNHFI PQPGEEGDETGWNDFEARWMT	
Sbjct	181	IVANGVIVAGSTCQYSPYGC FISGHSATGEELWRNHFI PQPGEEGDETGWNDFEARWMT	240

Query	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
		GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	
Sbjct	241	GVWGQITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT	300
Query	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDAA	360
		PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDAA	
Sbjct	301	PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDAA	360
Query	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD	420
		SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD	
Sbjct	361	SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD	420
Query	421	TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAI DISTGRTLWSA	480
		TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAI DISTGRTLWSA	
Sbjct	421	TGIYFLPLNNACYDIMAVDQEFSSALDVYNTSATAKLAPGFENMGRIDAI DISTGRTLWSA	480
Query	481	ERPAANYSPVLSTAGGVVFNGGTD RYFRALSQETGETLWQARLATVATGQAISYELDG VQ	540
		ERPAANYSPVLSTAGGVVFNGGTD RYFRALSQETGETLWQARLATVATGQAISYELDG VQ	
Sbjct	481	ERPAANYSPVLSTAGGVVFNGGTD RYFRALSQETGETLWQARLATVATGQAISYELDG VQ	540
Query	541	YIAIGAGGLTYGTQLN	556
		YIAIGAGGLTYGTQLN	
Sbjct	541	YIAIGAGGLTYGTQLN	556

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation Align

Sequence 1: unnamed protein product

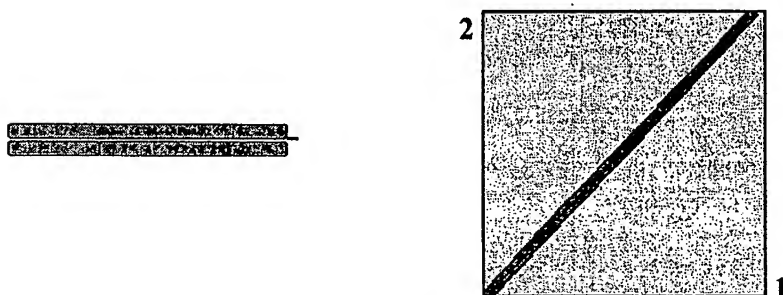
Length = 579 (1 .. 579)

Sequence 2: unnamed protein product

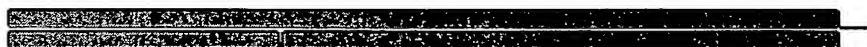
Length = 555 (1 .. 555)

1: B

2: sb



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1015 bits (2624), Expect = 0.0

Identities = 483/556 (86%), Positives = 516/556 (92%), Gaps = 1/556 (0%)

Query	1	MNPTLLRTSAVLLLTAPAAFAQVTPITDELLANPPAGEWINYGRNQENYRHSPLTQIT	60
		M PT+LL SA L L A AFAQVTP+TDELLANPPAGEWI+YG+NQENYRHSPLTQIT	
Sbjct	1	MKPTSLLWASAGALALLAAPAFQVTPVTDELLANPPAGEWISYGQNQENYRHSPLTQIT	60
Query	61	ADNVGQLQLVWARGMEAGAVQVTPMIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
		+NVGQLQLVWARGM+ G VQVTP+IHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	
Sbjct	61	TENVGQLQLVWARGMQPGKVQVTPLIHDGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA	120
Query	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTGP	180
		VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTG	
Sbjct	121	VATLNAQGDRKRGVALYGTSLYFSSWDNHLIALDMETGQVVDVERGSGEDGLTSNTTG-	179
Query	181	IVANGVIVAGSTCQYSPYGCFIGHDSATGEELWRNHFIQPGEEGDETGWGNDFEARWMT	240
		IVANGVIVAGSTCQYSP+GCF+SGHDSATGEELWRN+FIP+ GEEGDETGWGNDFEARWMT	
Sbjct	180	IVANGVIVAGSTCQYSPFGCFVSGHDSATGEELWRNYFIPRAGEEGDETGWGNDFEARWMT	239

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Query  241  GVWQGITYDPVTNLVFGSTGVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT  300
          G  WGQITYDPVTNLV  YGST  VGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT
Sbjct  240  GAWGQITYDPVTNLVHYGSTAVGPASETQRGTPGGTLYGTNTRFAVRPDTGEIVWRHQT  299

Query  301  PRDNWDQECTFEMMVANVDVQPSAEMEGLRAINPNAATGERRVLTGAPCKTGTMWSFDA  360
          PRDNWDQECTFEMMV  NVDVQPS  EMEGL++INPNAATGERRVLTG  PCKTGTMW  FDA
Sbjct  300  PRDNWDQECTFEMMVTVNDVQPSTEMEGLQSINPNAATGERRVLTGVPCKTGTMWQFDAE  359

Query  361  SGEFLWARDTNYTNMIASIDETGLVTVNEDAVLKELDVEYDVCPTFLGGRDWSSAALNP  420
          +GEFLWARDTNY  NMI  SIDE  G+VTVNEDA+LKELDVEYDVCPTFLGGRDW  SAALNP
Sbjct  360  TGEFLWARDTNYQNMIESIDENGIVTVNEDAILKELDVEYDVCPTFLGGRDWPSAALNP  419

Query  421  TGIYFLPLNNACYDIMAVDQEFSA LDVYNTSATAKLAPGFENMGRIDAIDISTGRTLWS  480
          +GIYF+PLNN  CYD+MAVDQEF+++DVYNTS  KL PG + +GRIDAIDISTGRTLWS
Sbjct  420  SGIYFIPLNNVCYDMMAVDQEFSTMDVYNTSNVTKLPPGKDMIGRIDAIDISTGRTLWSV  479

Query  481  ERPAANYSPVLSTAGGVVFNGGTD RYFRALSQETGETLWQARLATVATGQAISYELDG  540
          ER  AANYSPVLST  GGV+FNNGGTD RYFRALSQETGETLWQ  RLATVA+GQAISYE+DG+Q
Sbjct  480  ERAAANYSPVLSTGGGVLFNGGTD RYFRALSQETGETLWQTRLATVASGQAISYEVDGM  539

Query  541  YIAIGAGGLTYGTQLN  556
          Y+AI  GG++YG+  LN
Sbjct  540  YVAIAGGGVSYGSGLN  555
```

CPU time: 0.04 user secs. 0.03 sys. secs 0.07 total secs.